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TABLE 1

MPPKTPRKTAATAAAAAAEPAPPPPPPPEEDPE	(34)
QDSGPEDPLPLVRLEFEETEEDFTALCQKLKIPDHVRERA	(74)
WLTWEKVSSVDGVLGYYIQKKKELWGICIFIAAVDLDEM	(114)
FTFTTELQKNIEISVHKFFNLKEIDTSTKVDNAMSRLKK	(154)
YDVLFALFSKLERTCELIYLTPSSSISTEINSALVLKVS	(194)
WITFLLAKEVQLQMEDDLVISFQLNCVLDYFIKLSPPML	(234)
LKEPYKTAVIPIINGSPTPRRGQMRSARIAKQLENDTRII	(274)
EVLCKEHENCNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV	(314)
ENLSKRYEEIYLKNKDLDARLFLDHDKTLQTDSIDSFETQ	(354)
RTPRKSNLDEEVNVIPPHTPVRTVMNTIQQLMMILNSASD	(394)
QPSENLISYFNNCTVNPKESILKRVKDIFYIFKEKFAKAV	(434)
GQGCVEIGSQRYKLGVRLYYRVMESMLKSEEERLSIQNFS	(474)
KLLNDNIFHMSLLACALEVVMATYSRSTSQNLDGTDSL	(514)
PWILNVNLKAFDFYKVIESTFIKAEGNLTREMIKHLCER	(554)
HRIMESLAWLSDSPLFDLIKQSKDRGPTDHLESACPLNL	(594)
PLQNNHTAADMYLSPVRSPKKKGSTRVNSTANAETQATS	(634)
AFQTQKPLKSTSLSLFYKKVYRLAYLRLNTLCERLLSEHP	(674)
ELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYGICKV	(714)
KNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEYDSIIV	(754)
FYNSVFMQRLLTNILQYASTRPPTLSPIPHIPRSPYKFPS	(794)
SPLRIPGGNIYISPLKSPYKISEGLPTPTKMTPRSRLV	(834)
IGESFGTSEKFQKINQMVCNSDRVLRSAEGSNPPKPLKK	(874)
LRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ	(914)
KMNDSDMTSNKEEK	(928)

single-letter abbreviations for the amino acid residues are:
A, Ala; C, Cys; D, Asp; E, Gly; F, Phe; G, Gly; H, His;
I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;
R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.--

Please replace paragraph [153] beginning at page 27, line 15, with the following:

[153] --The amino acid sequence (Table 1; SEQ ID NO:2) is written in the abbreviation code recognized in the art. Single-letter abbreviations for the amino acid residues are: A = Alanine, C = Cysteine, D = Aspartic acid, E = Glutamic Acid, F = Phenylalanine, G = Glycine, H = Histidine, I = Isoleucine, K = Lysine, L = Leucine, M = Methionine, N =

Asparagine, P = Proline, Q = Glutamine, R = Arginine, S = Serine, T = Threonine, V = Valine, W = Tryptophane and Y = Tyrosine.--

Please replace paragraph [225] beginning at page 27, line 15, with the following:

[225] --Pending U.S. patent application Serial No. 108,748 discloses and claims the RB gene and its clone. The RB gene and its clone had the nucleotide and amino acid sequences sequence depicted in Table 4 Table 2 (SEQ ID NOS:1 and 2).

TABLE 4

TTCCGGTTTT	TCTCAGGGGA	CGTTGAAATT	ATTTTGTA	CGGGAGTCGG	GAGAGGACGG	60
GGCGTGC	CCCC	GCGTGC	GCG	CGTCG	CCTCCACAGC	120
CCGCCGCGGA	AAGGC	GTC	ATG	CCG	CCC	171
	Met	Pro	Pro	Lys	Thr	Pro
					Arg	Lys
					Thr	Ala
						Ala
1			5			10
ACC	GCC	GCC	GCT	GCC	GCG	219
Thr	Ala	Ala	Ala	Ala	Glu	Pro
15	20	25				
CCT	CCT	GAG	GAG	GAC	CCA	267
Pro	Pro	Glu	Glu	Asp	Pro	Glu
30	35	40				
CTC	GTC	AGG	CTT	GAG	TTT	315
Leu	Val	Arg	Leu	Glu	Glu	Asp
45	50	55				
TTA	TGT	CAG	AAA	TTA	AAG	363
Leu	Cys	Gln	Lys	Leu	Lys	Ile
60	65	70	75			
TTA	ACT	TGG	GAG	AAA	GTT	411
Leu	Thr	Trp	Glu	Lys	Val	Ser
80	85	90				
ATT	CAA	AAG	AAA	AAG	GAA	459
Ile	Gln	Lys	Lys	Glu	Leu	Trp
95	100	105				
GTT	GAC	CTA	GAT	GAG	ATG	507
Val	Asp	Leu	Asp	Glu	Met	Ser
110	115	120				

ATA GAA ATC AGT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp	555
125 130 135	
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr	603
140 145 150 155	
GAT GTA TTG TTT GCA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu	651
160 165 170	
ATA TAT TTG ACA CAA CCC AGC AGT TCG ATA TCT ACT GAA ATA AAT TCT Ile Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser	699
175 180 185	
GCA TTG GTG CTA AAA GTT TCT TGG ATC ACA TTT TTA TTA GCT AAA GGG Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly	747
190 195 200	
GAA GTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met	795
205 210 215	
CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu	843
220 225 230 235	
AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg	891
240 245 250	
ACA CCC AGG CGA GGT CAG AAC AGG AGT GCA CGG ATA GCA AAA CAA CTA Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu	939
255 260 265	
GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys	987
270 275 280	
AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe	1035
285 290 295	
ATG AAT TCT CTT GGA CTT GTA ACA TCT AAT GGA CTT CCA GAG GTT GAA Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu	1083
300 305 310 315	
AAT CTT TCT AAA CGA TAC GAA ATT TAT CTT AAA AAT AAA GAT CTA Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu	1131
320 325 330	

GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT	1179
<u>Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser</u>	
335 340 345	
<hr/>	
ATA GAC AGT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT	1227
<u>Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp</u>	
350 355 360	
<hr/>	
GAA GAG GTG AAT GTA ATT CCT CCA CAC ACT CCA GTT AGG ACT GTT ATG	1275
<u>Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met</u>	
365 370 375	
<hr/>	
AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT GAT CAA	1323
<u>Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln</u>	
380 385 390 395	
<hr/>	
CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA	1371
<u>Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro</u>	
400 405 410	
<hr/>	
AAA GAA AGT ATA CTG AAA AGA GTG AAG GAT ATA GGA TAC ATC TTT AAA	1419
<u>Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys</u>	
415 420 425	
<hr/>	
GAG AAA TTT GCT AAA GCT GTG GGA CAG GGT TGT GTC GAA ATT GGA TCA	1467
<u>Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser</u>	
430 435 440	
<hr/>	
CAG CGA TAC AAA CTT GGA GTT CGC TTG TAT TAC CGA GTA ATG GAA TCC	1515
<u>Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser</u>	
445 450 455	
<hr/>	
ATG CTT AAA TCA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA	1563
<u>Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys</u>	
460 465 470 475	
<hr/>	
CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG GCG TGC GCT CTT	1611
<u>Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu</u>	
480 485 490	
<hr/>	
GAG GTT GTA ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT	1659
<u>Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp</u>	
495 500 505	
<hr/>	
TCT GGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA	1707
<u>Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu</u>	
510 515 520	
<hr/>	
AAA GCC TTT GAT TTT TAC AAA GTG ATC GAA AGT TTT ATC AAA GCA GAA	1755
<u>Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu</u>	
525 530 535	

GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT	1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His	
540 545 550 555	
CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT	1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp	
560 565 570	
CTT ATT AAA CAA TCA AAG GAC CGA GAA GGA CCA ACT GAT CAC CTT GAA	1899
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu	
575 580 585	
TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA	1947
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala	
590 595 600	
GAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GGT TCA ACT	1995
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr	
605 610 615	
ACG CGT GTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TCA GCC	2043
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala	
620 625 630 635	
TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT	2091
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr	
640 645 650	
AAA AAA GTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA	2139
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu	
655 660 665	
CGC CTT CTG TCT GAG CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT	2187
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu	
670 675 680	
TTC CAG CAC ACC CTG CAG AAT GAG TAT GAA CTC ATG AGA GAC AGG CAT	2235
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His	
685 690 695	
TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT GGC ATA TGC AAA GTG AAG	2283
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys	
700 705 710 715	
AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG GAT CTT	2331
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu	
720 725 730	
CCT CAT GCT GTT CAG GAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG	2379
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu	
735 740 745	
GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA	2427

Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg			
750	755	760	
CTG AAA ACA AAT ATT TTG CAG TAT GCT TCC ACC AGG CCC CCT ACC TTG		2475	
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu			
765	770	775	
TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA		2523	
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser			
780	785	790	795
CCC TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAG AGT		2571	
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser			
800	805	810	
CCA TAT AAA ATT TCA GAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA		2619	
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro			
815	820	825	
AGA TCA AGA ATC TTA GTA TCA ATT GGT GAA TCA TTC GGG ACT TCT GAG		2667	
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu			
830	835	840	
AAG TTC CAG AAA ATA AAT CAG ATG GTA TGT AAC AGC GAC CGT GTG CTC		2715	
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu			
845	850	855	
AAA AGA AGT GCT GAA GGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA		2763	
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu			
860	865	870	875
CGC TTT GAT ATT GAA GGA TCA GAT GAA GCA GAT GGA AGT AAA CAT CTC		2811	
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu			
880	885	890	
CCA GGA GAG TCC AAA TTT CAG CAG AAA CTG GCA GAA ATG ACT TCT ACT		2859	
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr			
895	900	905	
CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA		2907	
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser			
910	915	920	
AAC AAG GAA GAG AAA TGAGGATCTC AGGACCTTGG TGGACACTGT GTACACCTCT		2962	
Asn Lys Glu Glu Lys			
925			
GGATTCAATTG TCTCTCACAG ATGTGACTGT AT		2994	

TABLE 4

TTCCCCGTTTT TCTCAGGGCA CGTTGAAATT ATTTTTGTAA CGGGACTCGG GAGAGGACGG 60
CCCGTCCCCC CCCTCCCCCC CGCTCCCTCTT CCCCCGGGCT CCTCCACAGC TGGCTGGCTC 120
CCCCGGGGA AAGGGCTC ATG CCC CCC AAA ACC CCC CCA AAA ACC CCC CCC 171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
1 5 10
ACC CCC CCC CCT GCC CCC GAA CCC CCG GCA CCG CCC CCG CCC CCC 219
Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
15 20 25
CCT CCC TAG GAG GAC CCA GAG GAC AGC CCC CCC GAG GAC CTG CCT 267
Pro Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro
30 35 40
CTC CTC ACC CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA 315
Leu Val Arg Leu Glu Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
45 50 55
TTA TCT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA GAG AGA GCT TGC 363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60 65 70 75
TTA ACT TGG CAC AAA CTT TCA TCT CTC GAT CGA GTA TTG CGA CGT TAT 411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
80 85 90
ATT CAA AAG AAA AAG GAA CTG TGG CGA ATC TGT ATC TTT ATT GCA GCA 459
Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
95 100 105
GTT GAC CTA GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC 507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Cys Lys Asn
110 115 120
ATA GAA ATC ACT GTC CAT AAA TTC TTT AAC TTA CTA AAA CAA ATT GAT 555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
125 130 135
ACC AGT ACC AAA GTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAG TAT 603
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
140 145 150 155
GAT CTA TTC TTT CGA CTC TTC AGC AAA TTG GAA AGG ACA TGT GAA CTT 651
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
160 165 170

ATA TAT TTG ACA CAA CCC ACC ACT TCG ATA TCT ACT GAA ATA AAT TCT 699
 Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
 175 180 185

GCA TTC GTG CTA AAA CTT TCT TGG ATC ACA TTT TTA TTA GCT AAA CGG 747
 Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
 190 195 200

GAA CTA TTA CAA ATG GAA GAT GAT CTG GTG ATT TCA TTT CAG TTA ATG 795
 Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
 205 210 215

CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC 843
 Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
 220 225 230 235

AAA CAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA 891
 Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
 240 245 250

ACA CCC AGG CGA GGT CAG AAC AGG ACT CCA CCC ATA CCA AAA CAA CTA 939
 Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
 255 260 265

GAA AAT GAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT 987
 Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
 270 275 280

AAT ATA GAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT 1035
 Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
 285 290 295

ATG AAT TCT CTT CGA CTT CTA ACA TCT AAT CCA CTT CCA GAG GTT GAA 1083
 Met Asn Ser Leu Cys Leu Val Thr Ser Asn Cys Leu Pro Glu Val Glu
 300 305 310 315

AAT CTT TCT AAA CGA TAC GAA GAA ATT TAT CTT AAA AAT AAA GAT CTA 1131
 Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
 320 325 330

GAT CGA AGA TTA TTT TTG CAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179
 Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
 335 340 345

ATA GAC ACT TTT GAA ACA CAG AGA ACA CCA CGA AAA ACT AAC CTT CAT 1227
 Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp
 350 355 360

GAA CAC GTC AAT GTA ATT CCT CCA CAC ACT CCA CTT AGG ACT GTP ATG 1275
 Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
 365 370 375

AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT CAT CAA 1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
380 385 390 395

CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTC AAT CCA 1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
400 405 410

AAA GAA ACT ATA CTG AAA AGA GTG AAC GAT ATA CGA TAG ATC TTT AAA 1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys
415 420 425

GAC AAA TTT CCT AAA GCT CTG CGA CAG GGT TGT GTC GAA ATT CGA TCA 1467
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser
430 435 440

CAC CGA TAC AAA CTT CGA CTT CGC TTG TAT TAC CGA GTC ATG CAA TCC 1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser
445 450 455

ATG CTT AAA TCA GAA GAA CGA TTA TCC ATT CAA AAT TTT AGC AAA 1563
Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys
460 465 470 475

CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG CGC TGC CCT CTT 1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu
480 485 490

GAC GTT CTA ATG GCC ACA TAT ACC AGA ACT ACA TCT CAG AAT CTT GAT 1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp
495 500 505

TCT CGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTG CTT AAT TTA 1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu
510 515 520

AAA CCC TTT GAT TTT TAC AAA CTG ATC CAA AGT TTT ATC AAA CGA CAA 1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu
525 530 535

CCC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT 1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His
540 545 550 555

CGA ATC ATG GAA TCC CTT CGA TGG CTC TCA CAT TGA CCT TTA TTT GAT 1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
560 565 570

CTT ATT AAA CAA TCA AAG GAC CGA GAA CGA CCA ACT GAT CAC CTT GAA 1899
Leu Ile Lys Gln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
575 580 585

TCT CCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA 1947
Ser Ala Cys Pro Leu Asn Leu Pro Leu Glu Asn Asn His Thr Ala Ala
590 595 600

GAT ATG TAT CTT TCT CCT CTA AGA TCT CCA AAG AAA AAA CGT TCA ACT 1995
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
605 610 615

ACG CGT CTA AAT TCT ACT GCA AAT GCA CAG ACA CAA CCA ACC TCA CCC 2043
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Glu Ala Thr Ser Ala
620 625 630 635

TTC CAG ACC CAC AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT 2091
Phe Glu Thr Glu Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
640 645 650

AAA AAA CTG TAT CGG CTA CCC TAT CTC CGG CTA AAT ACA CTT TGT GAA 2139
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
655 660 665

CGC CTT CTG TCT GAG CAC CCA CAA TTA CAA CAT ATC ATC TGG ACC CTT 2187
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
670 675 680

TTC CAG CAC ACC CTG CAG AAT CAG TAT CAA CTC ATG AGA GAC AGG CAT 2235
Phe Glu His Thr Leu Glu Asn Glu Tyr Glu Leu Met Arg Asp Arg His
685 690 695

TTG GAC CAA ATT ATC ATG TGT TCC ATG TAT CCC ATA TCC AAA CTG AAC 2283
Leu Asp Glu Ile Met Met Cys Ser Met Tyr Glu Ile Cys Lys Val Lys
700 705 710 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT CTA ACA GCA TAC AAG GAT CTT 2331
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
720 725 730

CCT CAT GCT GTT CAG CAG ACA TTC AAA CGT GTT TTG ATC AAA GAA GAG 2379
Pro His Ala Val Glu Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
735 740 745

GAG TAT GAT TCT ATT ATA CTA TTG TAT AAC TCC GTC TTC ATG CAG AGA 2427
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Glu Arg
750 755 760

CTG AAA ACA AAT ATT TTG CAG TAT CCT GCT TCC ACC AGG CCC CCT ACC TTG 2475
Leu Lys Thr Asn Ile Leu Glu Tyr Ala Ser Thr Arg Pro Pro Thr Leu
765 770 775

TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA 2523
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
780 785 790 795

ccc TTA CGG ATT CCT GGA GGG AAC ATC TAT ATT TCA CCC CTG AAC ACT 2571
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
800 805 810

cca TAT AAA ATT TCA CAA GGT CTG CCA ACA CCA ACA AAA ATG ACT CCA 2619
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
815 820 825

aga TCA AGA ATC TTA CTA TCA ATT CGT CAA TCA TTC GGG ACT TCT GAG 2667
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
830 835 840

aac TTC CAC AAA ATA AAT CAG ATG CTA TGT AAC ACC GAC CGT GTG CTC 2715
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
845 850 855

aaa AGA ACT CCT GAA CGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA 2763
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
860 865 870 875

ccc TTT CAT ATT GAA CGA TCA CAT CAA CCA GAT GGA ACT AAA CAT CTC 2811
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
880 885 890

cca CGA GAG TCC AAA TTT CAG CAG AAA CTC GCA GAA ATG ACT TCT ACT 2859
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
895 900 905

cga ACA CGA ATG CAA AAG CAG AAA ATG AAT CAT AGC ATG GAT ACC TCA 2907
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
910 915 920

aac AAG GAA GAG AAA TGACGGATCTC AGGACCTTGG TGGACACTGT CTAGACCTCT 2962
Asn Lys Glu Glu Lys
925

GGATTCAATTG TCTCTCACAG ATCTGACTGT AT 2994

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Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 10, at the end of the application.

In the Claims:

Please amend claims 35, 39 and 40 as follows:

1. (Original) A method of controlling cancer suppression in a mammal having a cancer suppressing gene, comprising the steps of:

making a substantially duplicated genetic material corresponding to the genetic material of said gene, the substantially duplicated material selected from the group consisting of a cloned cancer suppressing gene, a modified or defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof; and

interchanging said duplicated genetic material and the cancer suppressing gene of the mammal.

2. (Original) A method of claim 1, wherein before said making a substantially duplicated genetic material, determining the chromosomal location of said cancer suppressing gene of the mammal.

3. (Original) A method of claim 1, wherein after said making a substantially duplicated genetic material, detecting the presence or absence of an inactive cancer suppressing gene of a tissue sample of the mammal to determine whether or not the tissue sample cancer suppressing gene is defective or absent.

4. (Original) A method of claim 3, wherein in response to a determination that the tissue sample cancer suppressing gene is either defective or absent, replacing a cancer suppressing gene of the mammal with its clone.

5. (Original) A method of claim 3, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by measuring the amount of protein product of said cancer suppressing gene, of the tissue sample, bound by an antibody specific for said protein.

6. (Original) A method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by:

- (a) labeling said tissue sample with radioactive isotope;
- (b) lysing the labeled tissue;
- (c) reacting the protein product of said cancer suppressing gene with an antibody specific for said protein thereby forming a protein/antibody immunocomplex;
- (d) autoradiographing the immunocomplex obtained in step (c); and
- (e) determining the presence or absence of the protein product by comparing the autoradiogram of step (d) with the autoradiogram of the standard protein product.

7. (Original) The method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by enzyme immunoassay techniques.

8. (Original) The method of claim 5, wherein the determination of whether or not the tissue sample cancer suppressing gene is defective or absent is accomplished by immunocytochemistry methods.

9. (Original) The method of claim 5, wherein the cancer suppressing gene is the RB gene and the protein product is ppRB¹¹⁰.

10. (Original) The method of claim 1, wherein said cancer suppressing gene is replaced with substantially duplicated material selected from the group consisting of said cloned cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof, for therapeutic purposes.

11. (Original) The method of claim 1, wherein said cancer suppressing gene is replaced with substantially duplicated material selected from the group consisting of said defective cancer suppressing gene, homologues thereof, fragments thereof, and mixtures thereof, for facilitating the testing of the carcinogenicity of environmental influences.

12. (Original) The method of claim 2, wherein the location of said cancer suppressing gene is determined by chromosome walking.

13. (Original) The method of claim 2, wherein the location of said cancer suppressing gene is determined through organic markers.

14. (Original) A method of claim 2, wherein:
said chromosomal location of said cancer suppressing gene is determined by testing genes of a chromosome for phenotypic expression;
determining one of the genes of said chromosome to be a marker gene; and
using chromosomal walking techniques to locate a cancer suppressing gene.

15. (Original) An animal genetically altered so as to have the allele of at least one cancer suppressing gene selected from the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a mixture thereof.

16. (Original) An animal of claim 15, wherein said defective allele is selected from the group consisting of defective alleles of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues thereof, fragments thereof, and mixtures thereof.

17. (Original) An animal of claim 15, wherein said allele contains a DNA fragment having at least one defective nucleotide sequence.

18. (Original) An animal of claim 15, wherein said defective allele contains a DNA fragment having at least one defective RB nucleotide sequence.

19. (Original) The animal of claim 15, wherein said animal is a mouse.

20. (Original) A method for determining the carcinogenicity of suspected environmental influences, using the animal of claim 14, comprising the steps of:
exposing said animal to a suspected environmental influence;
observing the animal for the phenotypic expression of cancer; and
determining carcinogenicity of the suspected environmental influence in response to observing a phenotypic expression of cancer in the animal.

21. (Original) A method of claim 20, wherein said exposing includes exposing to a source of radiation.

22. (Original) A method of claim 20, wherein said exposing includes exposing to tobacco combustion products.

23. (Original) A method of claim 20, wherein said exposing includes exposing to food additives.

24. (Original) A method of claim 20, wherein said exposing includes exposing to artificial substances.

25. (Original) A method of claim 20, wherein said observing includes examining the animal for tumor development.

26. (Original) A method of claim 25, wherein in response to the formation of a tumor in the animal, analyzing the tumor for the presence of cancer cells.

27. (Original) A method of making the animal of claim 15, comprising:
using at least one allele of an animal cancer suppressing gene selected from the group consisting of a defective allele, a homologue thereof, a fragment thereof, and a mixture thereof;

mutating at least one animal cell with said allele to form a mutated cell;
introducing said mutated cell into an animal blastocyst;

permitting growth of the blastocyst for a given period of time sufficient to incorporate said allele into its cells; repressing genetic recombinations within said cells; transferring the blastocyst containing said allele into the uterus of a pseudo pregnant animal for giving birth subsequently to an animal bearing said allele;

breeding said animal to reproduce additional animals; and
selecting the animal of claim 14 from said additional animals by determining the presence therein of the said allele.

28. (Original) A method of claim 27, wherein before introducing said allele, removing said blastocyst from a super ovulated animal, and wherein said blastocyst is comprised of undifferentiated cells.

29. (Original) A method of claim 27, wherein said introducing is performed in vitro.

30. (Original) A pharmaceutical composition wherein the active ingredient is selected from the group consisting of a naturally occurring intact cancer suppressing gene, a cloned intact cancer suppressing gene, fragments thereof, homologues thereof and mixtures thereof.

31. (Original) A pharmaceutical composition of claim 30, wherein said naturally occurring and cloned cancer suppressing gene is selected from the group consisting of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, homologues thereof, fragments thereof, and mixtures thereof.

32. (Original) A pharmaceutical composition of claim 30, wherein the active ingredient is selected from the group consisting of RB cDNA, modified RB cDNA fragment, clones thereof, homologues thereof and mixtures thereof.

33. (Original) A pharmaceutical composition of claim 31, wherein the active ingredient for each of said gene is selected from the group consisting of cDNA of said gene, fragments of said cDNA, homologues thereof and mixtures thereof.

34. (Original) A pharmaceutical composition of claim 32, wherein the cancer suppressing gene is isolated from human chromosome 13 region 13q14.

35. (Currently amended) A pharmaceutical composition of claim 31, wherein the cancer suppressing gene and its clone each has the following nucleotide sequence comprising SEQ ID NO:1:

TTCGGGTTT TCTCAGGGGA CCTTGAAATT ATTTTGCTAA CCGGACTCCC CAGAGGACGG 60
CCCGTCCCCC CCCTCCCCCC CCTCGCTCT CCCCGGGCT CCTCCACACC TCCCTGGCTC 120
CCCCCCCCCA AACGGCTC ATG CCC CCC AAA ACC CCC CGA AAA ACC CCC CCC 171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
1 5 10
ACC CCC CCC CCT CCC CCC GAA CCC CCC CGA CCC CCC CCC CCC CCC 219
Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro
15 20 25
CCT CCG TAG GAG GAC CCA GAG CAC AGC ACC CCC CGG GAG GAC CTC CCT 267
Pro Pro Glu Glu Asp Pro Glu Cln Asp Ser Gly Pro Glu Asp Leu Pro
30 35 40
CTC GTC AGG CTT GAG TTT GAA GAA ACA GAA GAA CCT GAT TTT ACT GCA 315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
45 50 55
TTA TGT CAC AAA TTA AAC ATA CCA CAT CAT GTC ACA CAG ACA GCA GCT TGC 363
Leu Cys Cln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60 65 70 75
TTA ACT TGG GAG AAA GTT TCA TCT GTG GAT GCA CTA TTG GGA GGT TAT 411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
80 85 90
ATT CAA AAC AAA AAC GAA CTG TGG GGA ATC TGT ATC TTT ATT GCA GCA 459
Ile Cln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
95 100 105
GTT GAC CTA CAT GAT GAG ATG TCG TTC ACT TTT ACT GAG CTA CAG AAA AAC 507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Glu Leu Gln Lys Asn
110 115 120
ATA CAA ATC ACT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT GAT 555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
125 130 135

ACC ACT ACC AAA CTT GAT AAT GCT ATG TCA AGA CTC TTG AAC AAG TAT 603
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
140 145 150 155

GAT GCA TTC TTT GCA CTC TTC AGC AAA TTG CAA AGG ACA TGT GAA CTT 651
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
160 165 170

ATA TAT TTG ACA CAA CCC AGC AGT TCC ATA TCT ACT GAA ATA AAT TCT 699
Ile Tyr Leu Thr Gln Pro Ser Ser Ile Ser Thr Glu Ile Asn Ser
175 180 185

GCA TTG GTC CTA AAA CTT TCT TGG ATC ACA TTT TTA TTA CCT AAA CGG 747
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
190 195 200

GAA GCA TTA CAA ATG GAA CAT GAT CTG CTG ATT TCA TTT CAG TTA ATG 795
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
205 210 215

CTA TGT GTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATC TTG CTC 843
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
220 225 230 235

AAA GAA CCA TAT AAA ACA CCT CTT ATA CCC ATT AAT CGT TCA CCT CGA 891
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
240 245 250

ACA CCC ACC CGA GGT CAG AAC AGC AGT GCA CGG ATA GCA AAA GAA CTA 939
Thr Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
255 260 265

GAA AAT GAT ACA AGA ATT ATT CAA CTT CTC TGT AAA GAA CAT GAA TGT 987
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
270 275 280

AAT ATA GAT GAG GTG AAA AAT CTT TAT TTC AAA AAT TTT ATA CCT TTT 1035
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
285 290 295

ATG AAT TCT CTT CGA CTT GTC ACA TGT AAT CGA CTT CCA GAG CTT CGA 1083
Met Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
300 305 310 315

AAT CTT TCT AAA CGA TAC GAA ATT TAT CTT AAA AAT AAA GAT CTA 1131
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
320 325 330

GAT GCA AGA TTA TTT TTG GAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser
335 340 345

ATA GAC ACT TTT GAA ACA CAG AGA ACA CCA CGA AAA AGT AAC CTT GAT 1227
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp
350 355 360

GAA GAG GTC AAT CTA ATT CCT CCA CAC ACT CCA CTT AGG ACT CTT ATC 1275
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
365 370 375

AAC ACT ATC CAA CAA TTA ATC ATG ATT TTA AAT TCA GCA ACT GAT CAA 1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
380 385 390 395

CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TCC AGA CTG AAT CCA 1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
400 405 410

AAA GAA ACT ATA CTG AAA AGA CTG AAC GAT ATA GGA TAC ATC TTT AAA 1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys
415 420 425

GAG AAA TTT GCT AAA CCT CTC GGA CAG GGT TGT GTC GAA ATT GGA TCA 1467
Glu Lys Phe Ala Lys Ala Val Gly Cln Gly Cys Val Glu Ile Gly Ser
430 435 440

CAG CGA TAC AAA CTT CGA CTT CGC TTC TAT TAC CGA GTC ATG CAA TCC 1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser
445 450 455

ATC CTT AAA TCA CAA GAA CAA CGA TTA TCC ATT CAA AAT TTT AGC AAA 1563
Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys
460 465 470 475

CTT CTG AAT GAC AAC ATT TTT GAT ATG TCT TTA TTG GCG TGC CCT CTT 1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu
480 485 490

GAG CTT GTC ATG CCC ACA TAT AGC AGA ACT ACA TCT CAG AAT CTT CAT 1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Cln Asn Leu Asp
495 500 505

TCT CGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT CTG CTT AAT TTA 1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu
510 515 520

AAA CCC TTT GAT TTT TAC AAA GTG ATC GAA ACT TTT ATC AAA GCA GAA 1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu
525 530 535

GGC AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT 1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His
540 545 550 555

CGA ATC ATG GAA TCC CTT GCA TCG CTC TCA GAT TCA CCT TTA TTT GAT 1851
 Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
 560 565 570

CTT ATT AAA CAA TCA AAG GAC CGA GAA CGA CCA ACT GAT CAC CTT GAA 1899
 Leu Ile Lys Cln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
 575 580 585

TCT GCT TGT CCT CTT AAT CTT CCT CTC CAG AAT AAT CAC ACT GCA GCA 1947
 Ser Ala Cys Pro Leu Asn Leu Pro Leu Cln Asn Asn His Thr Ala Ala
 590 595 600

CAT ATG TAT CTT TCT CCT GTA AGA TCT CCA AAG AAA AAA GCT TCA ACT 1995
 Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
 605 610 615

ACC CGT CTA AAT TCT ACT GCA AAT GCA GAG ACA GAA GCA ACC TCA CCC 2043
 Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Cln Ala Thr Ser Ala
 620 625 630 635

TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTC TTT TAT 2091
 Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
 640 645 650

AAA AAA CTG TAT CCG CTA CCC TAT CTC CCG CTA AAT ACA CTT TGT GAA 2139
 Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
 655 660 665

CGC CTT CTG TCT GAC CAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT 2187
 Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
 670 675 680

TTC CAG CAC ACC CTG CAG AAT CAG TAT GAA CTC ATG ACA GAC ACC CAT 2235
 Phe Gln His Thr Leu Cln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
 685 690 695

TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT CGC ATA TGC AAA GTG AAC 2283
 Leu Asp Cln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
 700 705 710 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAG CAT CTT 2331
 Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
 720 725 730

CCT CAT CCT CTT CAG CAG ACA TTC AAA CGT CTT TTG ATC AAA GAA GAG 2379
 Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
 735 740 745

GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG AGA 2427
 Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg
 750 755 760

CTG AAA ACA AAT ATT TTC CAG TAT CCT TCC ACC ACC CCC CCT ACC TTG 2475
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu
765 770 775

TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT ACT TCA 2523
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
780 785 790 795

CCC TTA CGG ATT CCT CGA CGG AAC ATC TAT ATT TCA CCC CTC AAC AGT 2571
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
800 805 810

CCA TAT AAA ATT TCA GAA CGT CTG CCA ACA CCA ACA AAA ATG ACT CCA 2619
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
815 820 825

AGA TCA ACA ATC TTA GTC ATT CGT GAA TCA TTC CGG ACT TCT GAG 2667
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
830 835 840

AAC TTC CAG AAA ATA AAT CAG ATC GTC TGT AAC ACC CAC CGT GTG CTC 2715
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
845 850 855

AAA AGA ACT CCT CAA CGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA 2763
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
860 865 870 875

CGC TTT GAT ATT GAA CGA TCA GAT GAA CGA GAT CGA AGT AAA CAT CTC 2811
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
880 885 890

CCA CGA CAC TCC AAA TTT CAG CAG AAA CTC CGA GAA ATG ACT TCT ACT 2859
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
895 900 905

CGA ACA CGA ATG CAA AAG CAG AAA ATG AAT GAT AGC ATG GAT ACC TCA 2907
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
910 915 920

AAC AAG GAA GAG AAA TGAGGGATCTC AGGACCTTGG TGCACACTGT CTACACCTCT 2962
Asn Lys Glu Glu Lys
925

CCATTGATTC TCTCTCACAG ATGTGAETCT AT 2994

36. (Original) A pharmaceutical composition of claim 32, wherein said RB cDNA fragment is selected from the group consisting of RB-1, RB-2, RB-5, γ 79R8 and mixtures thereof.

37. (Original) A pharmaceutical composition of claim 32, wherein a resulting mRNA transcript of said RB cDNA fragment has 4.6 kb.

38. (Original) A pharmaceutical composition of claim 37, wherein the cloned genomic DNA has at least 27 exons.

39. (Currently amended) A pharmaceutical composition of claim 30, wherein the cloned RB cDNA transcribes into mRNA which translates in protein having an amino acid sequence comprising SEQ ID NO:2:

MPPKTPRKTAATAAAAAAEPAPPPPPPPEEDPE (3 4)
QDSCGPEDLPLVRLFEETEEDFTALCQKLKIPDHVRERA (7 4)
WLTWEKVSCVDGVLGGYIQKKKEWLGCICIFIAAVDLEM (1 1 4)
FTFTELQKNIEISVHKFFNLLKEIDTSTKVDNAMSRLKK (1 5 4)
YDVLFAFLFSKLERTCLELIYLTPSSSISTEINSALVLKVS (1 9 4)
WITFLLAKGEVLFQMEDDLVISFQLNLCVLDYFIKLSPPML (2 3 4)
LKEPYKTAVIPINGSPRTPRRCQMRSAARIAKQLENDTRII (2 7 4)
EVLCKEHECNIDEVKNVYFKNFIPFMNSLGLVTSNGLPEV (3 1 4)
ENLSKRYEEIYLKNKDLDARLFLHDHKTLQTDSIDSFETQ (3 5 4)
RTPRKSNLDEEVNVIPHTPVRTVMNTIQQLMMILNSASD (3 9 4)
QPSENLISYFNNCTVNPKESILKRVKDIGYIFKEKFAKAV (4 3 4)
GQCCVEIGSQRYKLGVRLYYRVMESMLKSEERLSIQNFS (4 7 4)
KLLNDNIFHMSLLACALEVVMATYSRSTSQNLDSCTDLSF (5 1 4)
PWILNVNLKAFDYKVIESFIKAEGNLTREMIKHGERCE (5 5 4)
HRIMESLAWSDSLFDLIKQSKDREGPTDHLEGACPLNL (5 9 4)
PLQNNHTAADMYLSPVRSPKKKGSTRVNSTANAETQATS (6 3 4)
AFQTQKPLKSTSLSIFYKKVYRLAYLRLNTLCERLLSEHP (6 7 4)
ELEHIIWTLFQHTLQNEYELMRDRHLDQIMMCSMYCICKV (7 1 4)
KNIDLKFKIIVTAYKDLPHAVQETFKRVLIKEEYDSIV (7 5 4)
FYNSVFMQRLLKTNILQYASTRPPTLSPIPHIPRSPPYKFPS (7 9 4)
SPLRIPGGNIVISPLKSPYKISEGILPTPTKMTPRSRLVLS (8 3 4)
ICESFGTSEKFQKINQMVNCNSDRVILKRSAEGSNPPKPLKK (8 7 4)
LRFDIEGSDEADGSKHLPGESKFQQKLAEMTSTRTRMQKQ (9 1 4)
KMNDSMDTSNKEEK (9 2 8)

single letter abbreviations for the amino acid residues are:
A, Ala; C, Cys; D, Asp; E, Asn; F, Phe; G, Gly; H, His;

~~I, Ile; K, Lys; L, Leu; M, Met; N, Asn; P, Pro; Q, Gln;~~
~~R, Arg; S, Ser; T, Thr; V, Val; W, Trp; and Y, Tyr.~~

40. (Currently amended) A DNA nucleotide sequence comprising SEQ ID NO:1.:

TTCCGGTTTT TCTCAGGGCA CGTTGAAATT ATTTTGTAAC CCGGACTCGG CAGAGGACGG 60
CCCCGTCCCC CGCTGGGGCC CGCTCGTCCT CCCCCGGGCT CCTCCACAGC TCGCTGGCTC 120
CCCCGGGGCA AACGGGTC ATG CCG CCC AAA ACC CCC CGA AAA ACG CCC CCC 171
Met Pro Pro Lys Thr Pro Arg Lys Thr Ala Ala
1 5 10
ACC CCC CCC GCT GCC CCC CCG GAA CCC CCG CGA CCG CCG CCG CCC 219
Thr Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro
15 20 25
CCT CCC TAG GAC GAC CCA GAG CAG GAC AGC CCC CGG GAC GAC CTG CCT 267
Pro Pro Glu Glu Asp Pro Glu Cln Asp Ser Gly Pro Glu Asp Leu Pro
30 35 40
CTC GTC AGG CTT GAG TTT GAA CAA ACA CAA GAA CCT CAT TTT ACT GCA 315
Leu Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala
45 50 55
TTA TGT CAG AAA TTA AAG ATA CCA GAT CAT GTC AGA CAC AGA CCT TGG 363
Leu Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp
60 65 70 75
TTA ACT TGG GAG AAA CTT TCA TCT GTG GAT GGA GTC TTG GGA CGT TAT 411
Leu Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr
80 85 90
ATT CAA AAG AAA AAG GAA CTC TGG GGA ATC TGT ATC TTT ATT GCA GCA 459
Ile Gln Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Ala
95 100 105
CTT GAC CTA GAT GAC ATC TCG TTC ACT TTT ACT GAC CTA CAG AAA AAC 507
Val Asp Leu Asp Glu Met Ser Phe Thr Phe Thr Glu Leu Gln Lys Asn
110 115 120
ATA GAA ATC ACT GTC CAT AAA TTC TTT AAC TTA CTA AAA GAA ATT CAT 555
Ile Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp
125 130 135

ACC ACT ACC AAA CTT GAT AAT GCT ATG TCA AGA CTG TTG AAG AAC TAT 603
Thr Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr
140 145 150 155

GAT GTA TTG TTT CCA CTC TTC ACC AAA TTG GAA AGG ACA TGT GAA CTT 651
Asp Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu
160 165 170

ATA TAT TTG ACA CAA CCC AGC ACT TCG ATA TCT ACT GAA ATA AAT TCT 699
Ile Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser
175 180 185

GCA TTG CTG CTA AAA GTT TCT TCG ATC ACA TTT TTA TTA CCT AAA CGG 747
Ala Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly
190 195 200

GAA GTA TTA CAA ATG GAA GAT GAT CTG CTG ATT TCA TTT CAG TTA ATG 795
Glu Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met
205 210 215

CTA TGT CTC CTT GAC TAT TTT ATT AAA CTC TCA CCT CCC ATG TTG CTC 843
Leu Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu
220 225 230 235

AAA GAA CCA TAT AAA ACA GCT GTT ATA CCC ATT AAT GGT TCA CCT CGA 891
Lys Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg
240 245 250

AGA CCC AGG CGA GGT CAG AAC AGG ACT CGA CGG ATA GCA AAA CAA CTA 939
Thr Pro Arg Arg Gly Cln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu
255 260 265

GAA AAT CAT ACA AGA ATT ATT GAA GTT CTC TGT AAA GAA CAT GAA TGT 987
Glu Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys
270 275 280

AAT ATA CAT GAG GTG AAA AAT GTT TAT TTC AAA AAT TTT ATA CCT TTT 1035
Asn Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe
285 290 295

ATG AAT TCT CTT GGA CTT GTC ACA TGT AAT CGA CTT CCA GAG CTT GAA 1083
Met Asn Ser Leu Cys Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu
300 305 310 315

AAT CTT TCT AAA CGA TAC GAA ATT TAT CTT AAA AAT AAA GAT CTA 1131
Asn Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu
320 325 330

GAT GCA AGA TTA TTT TTG CAT CAT GAT AAA ACT CTT CAG ACT GAT TCT 1179
Asp Ala Arg Leu Phe Leu Asp His Asp Lys Thr Leu Cln Thr Asp Ser
335 340 345

ATA GAC ACT TTT GAA ACA CAG AGA ACA CCA CGA AAA ACT AAC CTT CAT 1227
Ile Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp
350 355 360

GAA GAG CTG AAT GTC ATT CCT CCA CAC ACT CCA GTT AGC ACT CTT ATG 1275
Glu Glu Val Asn Val Ile Pro Pro His Thr Pro Val Arg Thr Val Met
365 370 375

AAC ACT ATC CAA CAA TTA ATG ATG ATT TTA AAT TCA GCA AGT CAT CAA 1323
Asn Thr Ile Gln Gln Leu Met Met Ile Leu Asn Ser Ala Ser Asp Gln
380 385 390 395

CCT TCA GAA AAT CTG ATT TCC TAT TTT AAC AAC TGC ACA GTG AAT CCA 1371
Pro Ser Glu Asn Leu Ile Ser Tyr Phe Asn Asn Cys Thr Val Asn Pro
400 405 410

AAA GAA ACT ATA CTG AAA AGA GTC AAC GAT ATA CGA TAC ATC TTT AAA 1419
Lys Glu Ser Ile Leu Lys Arg Val Lys Asp Ile Gly Tyr Ile Phe Lys
415 420 425

GAC AAA TTT CCT AAA CCT CTG GCA CAC CCT TGT CTC GAA ATT CGA TCA 1467
Glu Lys Phe Ala Lys Ala Val Gly Gln Gly Cys Val Glu Ile Gly Ser
430 435 440

CAG CGA TAC AAA CTT CGA GTT CGC TTG TAT TAC CGA GTC ATG GAA TCC 1515
Gln Arg Tyr Lys Leu Gly Val Arg Leu Tyr Tyr Arg Val Met Glu Ser
445 450 455

ATG CTT AAA TCA GAA GAA CGA TTA TCC ATT CAA AAT TTT ACC AAA 1563
Met Leu Lys Ser Glu Glu Arg Leu Ser Ile Gln Asn Phe Ser Lys
460 465 470 475

CTT CTG AAT GAC AAC ATT TTT CAT ATG TCT TTA TTG CGG TGG CCT CTT 1611
Leu Leu Asn Asp Asn Ile Phe His Met Ser Leu Leu Ala Cys Ala Leu
480 485 490

GAC GTT GTC ATG GCC ACA TAT AGC AGA AGT ACA TCT CAG AAT CTT GAT 1659
Glu Val Val Met Ala Thr Tyr Ser Arg Ser Thr Ser Gln Asn Leu Asp
495 500 505

TCT CGA ACA GAT TTG TCT TTC CCA TGG ATT CTG AAT GTC CTT AAT TTA 1707
Ser Gly Thr Asp Leu Ser Phe Pro Trp Ile Leu Asn Val Leu Asn Leu
510 515 520

AAA CCC TTT GAT TTT TAC AAA GTC ATC GAA ACT TTT ATC AAA GCA GAA 1755
Lys Ala Phe Asp Phe Tyr Lys Val Ile Glu Ser Phe Ile Lys Ala Glu
525 530 535

GCG AAC TTG ACA AGA GAA ATG ATA AAA CAT TTA GAA CGA TGT GAA CAT 1803
Gly Asn Leu Thr Arg Glu Met Ile Lys His Leu Glu Arg Cys Glu His
540 545 550

CGA ATC ATG GAA TCC CTT GCA TGG CTC TCA GAT TCA CCT TTA TTT GAT 1851
Arg Ile Met Glu Ser Leu Ala Trp Leu Ser Asp Ser Pro Leu Phe Asp
560 565 570

CTT ATT AAA CAA TCA AAG GAC CGA CAA GGA CCA ACT CAT CAC CTT GAA 1899
Leu Ile Lys Cln Ser Lys Asp Arg Glu Gly Pro Thr Asp His Leu Glu
575 580 585

TCT CCT TGT CCT CTT AAT CCT CTC CAG AAT AAT CAC ACT GCA CCA 1947
Ser Ala Cys Pro Leu Asn Leu Pro Leu Gln Asn Asn His Thr Ala Ala
590 595 600

GAT ATC TAT CTT TCT CCT CTA AGA TCT CCA AAG AAA AAA GGT TCA ACT 1995
Asp Met Tyr Leu Ser Pro Val Arg Ser Pro Lys Lys Lys Gly Ser Thr
605 610 615

ACG CGT CTA AAT TCT ACT GCA AAT GCA GAG ACA CAA GCA ACC TGA CCC 2043
Thr Arg Val Asn Ser Thr Ala Asn Ala Glu Thr Gln Ala Thr Ser Ala
620 625 630 635

TTC CAG ACC CAG AAG CCA TTG AAA TCT ACC TCT CTT TCA CTG TTT TAT 2091
Phe Gln Thr Gln Lys Pro Leu Lys Ser Thr Ser Leu Ser Leu Phe Tyr
640 645 650

AAA AAA CTG TAT CGG CTA GCC TAT CTC CGG CTA AAT ACA CTT TGT GAA 2139
Lys Lys Val Tyr Arg Leu Ala Tyr Leu Arg Leu Asn Thr Leu Cys Glu
655 660 665

CCC CTT CTG TCT GAG GAC CCA GAA TTA GAA CAT ATC ATC TGG ACC CTT 2187
Arg Leu Leu Ser Glu His Pro Glu Leu Glu His Ile Ile Trp Thr Leu
670 675 680

TTC CAC CAC ACC CTG CAG AAT CAG TAT GAA CTC ATG AGA GAC AGG CAT 2235
Phe Gln His Thr Leu Gln Asn Glu Tyr Glu Leu Met Arg Asp Arg His
685 690 695

TTG GAC CAA ATT ATG ATG TGT TCC ATG TAT CGC ATA TGC AAA CTG AAG 2283
Leu Asp Gln Ile Met Met Cys Ser Met Tyr Gly Ile Cys Lys Val Lys
700 705 710 715

AAT ATA GAC CTT AAA TTC AAA ATC ATT GTA ACA GCA TAC AAC GAT CTT 2331
Asn Ile Asp Leu Lys Phe Lys Ile Ile Val Thr Ala Tyr Lys Asp Leu
720 725 730

CCT CAT CCT GTT CAG GAG ACA TTC AAA CGT CTT TTG ATG AAA GAA GAG 2379
Pro His Ala Val Gln Glu Thr Phe Lys Arg Val Leu Ile Lys Glu Glu
735 740 745

GAG TAT GAT TCT ATT ATA GTA TTC TAT AAC TCG GTC TTC ATG CAG ACA 2427
Glu Tyr Asp Ser Ile Ile Val Phe Tyr Asn Ser Val Phe Met Gln Arg
750 755 760

CTG AAA ACA AAT ATT TTG CAG TAT CCT TCC ACC AGG CCC CCT ACC TTC 2475
Leu Lys Thr Asn Ile Leu Gln Tyr Ala Ser Thr Arg Pro Pro Thr Leu
765 770 775

TCA CCA ATA CCT CAC ATT CCT CGA AGC CCT TAC AAG TTT CCT AGT TCA 2523
Ser Pro Ile Pro His Ile Pro Arg Ser Pro Tyr Lys Phe Pro Ser Ser
780 785 790 795

CCC TTA CGG ATT CCT CGA CGG AAC ATC TAT ATT TCA CCC CTG AAG AGT 2571
Pro Leu Arg Ile Pro Gly Gly Asn Ile Tyr Ile Ser Pro Leu Lys Ser
800 805 810

CCA TAT AAA ATT TCA GAA CGT CTG CCA ACA CCA ACA AAA ATG ACT CCA 2619
Pro Tyr Lys Ile Ser Glu Gly Leu Pro Thr Pro Thr Lys Met Thr Pro
815 820 825

AGA TCA AGA ATC TTA GTC TCA ATT CGT GAA TCA TTC GGG ACT TCT CAG 2667
Arg Ser Arg Ile Leu Val Ser Ile Gly Glu Ser Phe Gly Thr Ser Glu
830 835 840

AAC TTC CAG AAA ATA AAT CAG ATG GTC TGT AAC ACC GAC CGT CTG CTC 2715
Lys Phe Gln Lys Ile Asn Gln Met Val Cys Asn Ser Asp Arg Val Leu
845 850 855

AAA AGA AGT CCT GAA CGA AGC AAC CCT CCT AAA CCA CTG AAA AAA CTA 2763
Lys Arg Ser Ala Glu Gly Ser Asn Pro Pro Lys Pro Leu Lys Lys Leu
860 865 870 875

CGG TTT CAT ATT GAA CGA TCA GAT GAA CGA GAT CGA AGT AAA CAT CTC 2811
Arg Phe Asp Ile Glu Gly Ser Asp Glu Ala Asp Gly Ser Lys His Leu
880 885 890

CCA CGG CAG TCC AAA TTT CAG CAG AAA CTG CGA GAA ATG ACT TCT ACT 2859
Pro Gly Glu Ser Lys Phe Gln Gln Lys Leu Ala Glu Met Thr Ser Thr
895 900 905

CCA ACA CGA ATC CAA AAG GAG AAA ATG AAT GAT ACC ATG GAT ACC TCA 2907
Arg Thr Arg Met Gln Lys Gln Lys Met Asn Asp Ser Met Asp Thr Ser
910 915 920

AAC AAC GAA CAG AAA TGAGGATCTC AGGACCTTGC TCCACACTGT GTACACCTCT 2962
Asn Lys Glu Glu Lys
925

GGATTCAATTG TCTCTCACAG ATGTGACTGT AT 2994

41. (Original) A method of therapeutically treating inactive, mutative or absent cancer suppressing genes comprising:

treating said inactive, mutative or absent cancer suppressing genes with at least a portion of intact cancer suppressing genes.

42. (Original) A method of claim 41, wherein said cancer suppressing genes are each a substance selected from the groups consisting of RB genes, breast cancer suppressing genes, Wilm's tumor suppressing genes, Beckwith-Wiedemann syndrome suppressing genes, bladder transitional cell carcinoma suppressing genes, neuroblastoma suppressing genes, small cell lung carcinoma suppressing genes, renal cell carcinoma suppressing genes, acoustic neuroma suppressing genes, colorectal carcinoma suppressing genes, and mixtures thereof.

43. (Original) A method of claim 41, wherein said treating includes:
treating said inactive, mutative or absent cancer suppressing gene with a substance selected from the group consisting of an RB gene, a portion of said gene, or a mixture thereof.

44. (Original) A method of claim 43, wherein said portion is selected from the group consisting of RB cDNA, RB cDNA fragment, homologues thereof and mixtures thereof.

45. (Original) The method of claim 41, wherein the intact cancer suppressing gene, or portion thereof, is delivered to the site of a tumor by means of a retrovirus.

46. (Original) A method of claim 41, wherein the intact cancer suppressing gene, or a portion thereof, is delivered to the site of a tumor by a liposome.

47. (Original) A method of claim 41, wherein the location of said cancer suppressing gene is determined by utilizing a genetic marker.